

- 1 -

SEQUENCE LISTING

<110> ZENECA LIMITED

<120> GST SEQUENCES FROM SOYBEAN AND THEIR USE IN THE PRODUCTION OF HERBICIDE RESISTANT PLANTS

<130> ZENECA CASE PPD50449/WO

<140>

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<150> GB9922346.3

<151> 1999-09-21

<160> 43

<170> PatentIn Ver. 2.0

<210> 1

<211> 499

<212> PRT

<213> Glycine max

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Met Ser Gln Pro Leu Thr Thr Asn Ser Val Leu Val Glu Glu Ala Ala
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Ala Asp Gly Asp Ser Ser Ala Ala Ala Pro Pro Leu Phe Asp Tyr His
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Arg Ile Asp Gln Lys Leu Leu Gln Asn Ile Val Tyr Asp Ala Leu Val
35 40 45

Trp Ser Thr Leu Asn Cys Leu Leu Val Gly Asp Lys Ser Val Gln Arg
50 55 60

Ser Gly Arg Val Pro Gly Val Gly Leu Val His Leu Pro Leu Ser Leu
65 70 75 80

Leu Pro Gly Pro Phe Pro Glu Ser His Trp Lys Gln Gly Cys Glu Leu
85 90 95

- 2 -

Ala Pro Ile Phe Asn Glu Leu Val Asp Arg Val Ser Leu Asp Gly Lys
100 105 110

Phe Leu Gln Glu Ser Leu Ser Arg Thr Lys Asn Ala Asp Glu Phe Thr
115 120 125

Ser Arg Leu Leu Asp Ile His Ser Lys Met Leu Gln Ile Asn Lys Lys
130 135 140

Glu Asp Ile Arg Met Gly Ile Val Arg Ser Asp Tyr Met Ile Asp Glu
145 150 155 160

Lys Thr Lys Ser Leu Leu Gln Ile Glu Met Asn Thr Ile Ser Thr Ser
165 170 175

Phe Ala Leu Ile Gly Cys Leu Met Thr Gly Leu His Lys Ser Leu Leu
180 185 190

Ser Gln Tyr Gly Lys Phe Leu Gly Leu Asn Ser Asn Arg Val Pro Ala
195 200 205

Asn Asn Ala Val Asp Gln Ser Ala Glu Ala Leu Ala Lys Ala Trp Ser
210 215 220

Glu Tyr Asn Asn Pro Arg Ala Ala Ile Leu Val Val Val Gln Val Glu
225 230 235 240

Glu Arg Asn Met Tyr Glu Gln His Tyr Ile Ser Ala Leu Leu Arg Glu
245 250 255

Lys His His Ile Arg Ser Ile Arg Lys Thr Leu Thr Glu Ile Asp Gln
260 265 270

Glu Gly Lys Ile Leu Pro Asp Gly Thr Leu Ser Val Asp Gly Gln Ala
275 280 285

Ile Ser Val Val Tyr Phe Arg Ala Gly Tyr Thr Pro Lys Asp Tyr Pro
290 295 300

Ser Glu Ser Glu Trp Arg Ala Arg Leu Leu Met Glu Gln Ser Ser Ala
305 310 315 320

Ile Lys Cys Pro Thr Ile Ser Tyr His Leu Val Gly Thr Lys Lys Ile

- 3 -

325

330

335

Gln Gln Glu Leu Ala Lys Pro Gly Val Leu Glu Arg Phe Val Glu Asn

340

345

350

Lys Asp His Ile Ala Lys Leu Arg Ala Cys Phe Ala Gly Leu Trp Ser

355

360

365

Leu Glu Asp Ser Asp Ile Val Lys Lys Ala Ile Glu Asn Pro Glu Leu

370

375

380

Phe Val Met Lys Pro Gln Arg Glu Gly Gly Asn Asn Ile Tyr Gly

385

390

395

400

Asp Glu Leu Arg Glu Thr Leu Leu Lys Leu Gln Glu Ala Gly Ser Gln

405

410

415

Glu Asp Ala Ala Tyr Ile Leu Met Gln Arg Ile Phe Pro Ala Thr Ser

420

425

430

Pro Ala Ile Leu Val Arg Asp Gly Asn Trp Asp Thr Gly His Val Ile

435

440

445

Ser Glu Ala Gly Ile Phe Gly Thr Tyr Leu Arg Asn Lys Asp Lys Ile

450

455

460

Ile Ile Asn Asn Glu Ser Gly Tyr Met Val Arg Thr Lys Ile Ser Ser

465

470

475

480

Ser Tyr Glu Gly Val Leu Pro Gly Phe Gly Val Val Asp Thr Val

485

490

495

Tyr Leu Thr

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<223> Description of Artificial Sequence: Protein

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Fragment

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Protein
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<210> 4

<211> 15
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<223> Description of Artificial Sequence: Protein
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<223> Description of Artificial Sequence: Protein
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<213> Glycine max

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- 6 -

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<212> PRT

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<400> 7

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1 5 10 15

Pro Phe Leu His Arg Val Gln Ile Ala Leu Lys Leu Lys Gly Val Glu

20 25 30

Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu

35 40 45

Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu

50 55 60

Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr

65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu

85 90 95

Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala

100 105 110

Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Ala Lys

115 120 125

Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly

130 135 140

Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val

145 150 155 160

Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser

165 170 175

Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His

180 185 190

- 7 -

Pro Val Val Asn Glu Val Met Pro Pro Lys Asp Gln Leu Phe Ala Tyr
195 200 205

Phe Lys Ala Arg Ala Gln Ser Phe Val Ala Lys Arg Lys Asn
210 215 220

<210> 8
<211> 235
<212> PRT
<213> Glycine max

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Tyr Ala Lys Arg Val Glu Leu Ala Leu Asn Phe Lys Gly Ile Pro Tyr
20 25 30

Glu Tyr Val Glu Glu Asp Leu Arg Asn Lys Ser Asp Leu Leu Leu Lys
35 40 45

Tyr Asn Pro Val His Lys Lys Val Pro Val Leu Val His Asn Gly Lys
50 55 60

Ala Ile Ala Glu Ser Met Val Ile Leu Glu Tyr Ile Asp Glu Thr Trp
65 70 75 80

Lys Asp Gly Pro Lys Leu Leu Pro Ser Asp Ser Tyr Lys Arg Ala Gln
85 90 95

Ala Arg Phe Trp Cys His Phe Ile Gln Asp Gln Leu Met Glu Ser Thr
100 105 110

Phe Leu Val Val Lys Thr Asp Gly Glu Ala Gln Gln Lys Ala Ile Asp
115 120 125

His Val Tyr Glu Lys Leu Lys Val Leu Glu Asp Gly Met Lys Thr Tyr
130 135 140

Leu Gly Glu Gly Asn Ala Ile Ile Ser Gly Val Glu Asn Asn Phe Gly
145 150 155 160

- 8 -

Ile Leu Asp Ile Val Phe Cys Ala Leu Tyr Gly Ala Tyr Lys Ala His
165 170 175

Glu Glu Val Ile Gly Leu Lys Phe Ile Val Pro Glu Lys Phe Pro Val
180 185 190

Leu Phe Ser Trp Leu Met Ala Ile Ala Glu Val Glu Ala Val Lys Ile
195 200 205

Ala Thr Pro Pro His Glu Lys Thr Val Gly Ile Leu Gln Leu Phe Arg
210 215 220

Leu Ser Ala Leu Lys Ser Ser Ser Ala Thr Glu
225 230 235

<210> 9

<211> 223

<212> PRT

<213> Glycine max

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Met Ala Glu Val Lys Leu His Gly Phe Trp Tyr Ser Pro Tyr Thr Leu
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20 25 30

Glu Glu Asp Arg Tyr Asn Lys Ser Leu Gln Leu Leu Glu Tyr Asn Pro
35 40 45

Val Tyr Lys Lys Thr Pro Val Leu Val His Asn Gly Lys Pro Leu Cys
50 55 60

Glu Ser Met Leu Ile Val Glu Tyr Ile Asp Glu Ile Trp Ala His Asn
65 70 75 80

Ser Leu Leu Pro Ala Asp Pro Tyr Glu Arg Ala Leu Ala Arg Phe Trp
85 90 95

Val Lys Tyr Ala Asp Asp Asp Met Phe Ser Ala Val Ile Ala Phe Phe
100 105 110

- 9 -

Leu Ser Asn Asn Asp Glu Glu Arg Glu Lys Ser Ile Glu Lys Ile Trp
 115 120 125

Glu His Leu Arg Val Val Glu Asn Gln Cys Phe Gly Asp Gln Lys Lys
 130 135 140

Phe Phe Gly Gly Asp Ile Ile Asn Ile Met Asp Ile Ala Phe Gly Ser
 145 150 155 160

Ile Phe Lys Ile Leu Val Val Ala Glu Asp Ile Leu Asp Ala Lys Val
 165 170 175

Leu Glu Asp Glu Lys Phe Pro His Leu His Ser Trp Tyr Asn Asn Phe
 180 185 190

Lys Asp Val Ala Val Ile Lys Glu Asn Leu Pro Asp His Glu Lys Met
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Val Ala Phe Ala Lys Phe Ile Arg Glu Lys Arg Leu Ala Cys Thr
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<210> 10

<211> 232

<212> PRT

<213> Glycine max

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Met Ala Glu Arg Asp Leu Arg Leu Leu Gly Ala Trp Phe Ser Pro Phe
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Ala Leu Arg Val Gln Ile Ala Leu Asn Leu Lys Gly Leu Asp Tyr Glu
 20 25 30

Val Val Glu Glu Thr Leu Asn Pro Lys Ser Glu Leu Leu Leu Lys Ser
 35 40 45

Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys Val
 50 55 60

Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Val Trp Ser
 65 70 75 80

- 10 -

Asn Asn Ala Leu Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn
85 90 95

Ala Arg Phe Trp Val Ser Tyr Ile Asp Asp Lys Trp Leu Thr Ser Leu
100 105 110

Lys Ser Val Leu Ala Thr Glu Asp Asp Glu Ala Lys Lys Leu His Phe
115 120 125

Glu Gln Ala Glu Glu Val Leu Glu Lys Val Glu Glu Val Phe Asn Lys
 130 135 140

Cys Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Thr Ile Gly Phe Val
145 150 155 160

Asp Ile Gly Phe Gly Ser Phe Leu Ser Phe Ile Arg Val Ser Glu Asn
165 170 175

Met Asn Glu Arg Lys Leu Leu Asp Glu Thr Lys Tyr Pro Gly Leu Thr
180 185 190

Leu Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Leu Leu
195 200 205

Trp Ala Ala Ala Ala Ala Ala Lys
225 230

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<211> 885
<212> DNA
<213> Glycine max

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tgcttgttca caatgagaag cccatttcag agtcccttgt gattgttgag tacattgtat 240  
acacatggaa aaacaatccc atcttgcctt ctgatcccta ccaaagagcc ttggctcgat 300  
tctgggctaa gttcattgtat gacaagtgtg tggttccagc atgaaatct gcttttatga 360
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- 11 -

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 ctgtttaat acctataatt caagagatag cagggtgc attgttcaca agtgagaaat 540
 tcccaaagct ctctaaatgg agccaagact ttcacaaacca tccagttgtc aacgaagtta 600
 tgcctcctaa ggatcaactt ttgcctatt tcaaggctcg ggctcaaagc ttcgttgcta 660
 aaagaaaagaa ttaatatagt gagactcaga atttccatcg aggtttcagt attgtatgaa 720
 atgaaagcta cttgtctatg tttcgattt gcggttgtat tttcattttt caatgaatta 780
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 tgagtcgtgt tagagcaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 885

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<211> 899

<212> DNA

<213> Glycine max

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 aataagagt atttgcttct aaagtacaac cctgttcaca agaagggtcc tgtacttggtt 180
 cataatggaa aggccattgc tgaatccatg gtgatcctt agtatattga tgaaacatgg 240
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<213> Glycine max

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 aaacccttat gtgagttccat gcttattgtt gaatacatttgc atgagatttgc ggcacataat 240
 tcattacttc ctgctgtatcc ctacgagaga gctctggcaa gttttgggt taaatatgct 300

- 12 -

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<211> 918

<212> DNA

<213> Glycine max

<400> 14

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ttcagtccat ttgccctgag ggtgcagatt gcccttaacc tcaagggttt ggattatgag 180
gttgttgaag agactttgaa tcccaaaagt gaattgcttc ttaagtccaa ccctgtgcac 240
aagaaaatcc cagtttctt ccatggagat aaagtcatat gtgaatctgc aatcatagtt 300
gagtagatag atgaggtttg gtccaaacaat gctctctcca tccttccaca aaatgcatat 360
gatcgagcta atgcccgtt tacatcgatg acaagtggct tacgtccttg 420
aaaagtgttc tagcgactga agatgatgag gcaaagaagc tacactttga gcaagcggaa 480
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aagcttgtt agtttgcaaa gattcttcag ctaaaatggg ctgctgcagc tgctgcaaag 780
taaatggaat caaattaatt gctggatgaa tttcaaaaat tgttgtgcaa gttatttata 840
tctgaggctt tggttggc aactttatatttaaaagt caaaataaat gttatgataa 900
tatagtaaaa aaaaaaaaaa 918

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

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<210> 16
<211> 23
<212> DNA
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<223> Description of Artificial Sequence:PRIMER

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23

<210> 17
<211> 27
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<400> 17
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<210> 18
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<210> 19
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:PRIMER

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23

<210> 20

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

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<210> 21

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

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<210> 22

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<212> DNA

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<223> Description of Artificial Sequence:PRIMER

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<210> 23

<211> 24

<212> DNA

- 15 -

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

<400> 23

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<210> 24

<211> 24

<212> DNA

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<223> Description of Artificial Sequence:PRIMER

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<210> 25

<211> 2763

<212> DNA

<213> Artificial Sequence

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nucleic acid sequence P32110

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gaaaatattt atataattac acaaaatctt aaaaaatgtt gttatttattt actactaatt 840

- 16 -

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<210> 26

<211> 1137

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mungbean
Sequence U20809

<400> 26

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aagggttccag tggttgtca tggtgacaaa ccccttccag agtcccttgt gattgttgag 240
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accaacaaga ttaagtaagg ctgcattatt tgtcttttg ttaaatttaga tattagtagt 960
cacaaaaaaag tgagtatttc cttacagaag ctttttaaat attaagttagt taattccata 1020
ggtctaccat tatagctcaa gttatataca tattatgggt gccattctct actcaacaat 1080
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<210> 27

<211> 2038

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Tobacco
sequence Q03663

<400> 27

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tataaaatatg gaagttaaaaa ttaatcgat cgttaaatgt agaaaatattt attaacaca 600
ttaaccataa ccagtctact ttatttaaca aaaagcacat ctgaratarc aaaaaagtgt 660
ttaacttcat gcattgacaa tttaaaaatta ttttgcacaa tcgggtaaaaa ctattttaca 720

- 18 -

acaattggta actgcatata taagtttaat atggtaacct agaaaaatagg ataaattatc 780
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<210> 28

<211> 2796

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Potato- Derived
nucleic acid sequence P32111

<400> 28

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aacccaactc aatattagaa aatcaaaaaat ttttagtgcatt tcatttataa aaaaaaaaaa 180
aattacttat gcagttcttgc aaccctttgt gagacgagag ggagttgctc ggatggtaag 240
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ggagctccta gaaagggtaa aaaaaaaaaa aaaaattaat aaaaaaatac cctttatgaa 360
atttctcatt ccgctactgc acttctcccc tgatcttccct cgtgtttca attattaattt 420
ctatattcat gacaccatgt gatgtttctc tgggttagtcc taaaaataga ggtattgaaa 480
attatgttgtt ttctctctgg tctatttact tttcttggtgt actttattgtt atttcatattt 540
gttaattttt ggcttcgttt tataacatgt tattagcaca aaactttaat catatcgagt 600

- 19 -

taaactttta attttgctta tcaacgtaaa agacaagata tgtgatcgac atgtataact 660
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tgtcgttaa ctttggagcg tacaagtgtc tacttgtat ccagtaggtt atcaaagctg 780
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<210> 29

<211> 1289

<212> DNA

<213> Artificial Sequence

- 20 -

<220>

<223> Description of Artificial Sequence:Arabidopsis

P46421

<400> 29

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caaagttcggtt cgtcggttta tcacaagacc atcaacacca taaggctata aatccaagct 240
aaaaggttgtt gattaactcc acaaaaccag aaaaactaca tttctaacat atagaagaaa 300
cagagaaaaa gagagagaga cccctaattgg ctgagaaaaga agaagtgaag cttttggga 360
tatggcgag cccttttagc cgtcgggtcg agatggctct caaactcaaa ggcataccgt 420
acgagttacgt ggaagagata ctggagaaca aaagccctt gcttcttgct cttaacccta 480
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gttgtgttgt tgagaagtga ggttttatca tcatctctca cgttatctta tttggccc 1260
gccactattt agaattaatg gtaaaagctt 1289

<210> 30

<211> 1339

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Arabidopsis

Genomic sequence

<400> 30

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agagataaaa aaaaattgtt taggaaacgt tataaatatg ttgtaaagtc aacatctgtt 180
tccttctaga ctcttcgcac ttacatcaca ctgccgacca tataaaacgg caaagttcggtt 240
cgtcgttttta tcacaagacc atcaacacca taaggctata aatccaagct aaaaggttgtt 300

gattaactcc acaaaaaccag aaaaaactaca tttctaacat atagaagaaa cagagaaaa 360
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caatgttgtt atggttatgt tggtgtttat tttattgaat atctttgtat gttgtgtgg 1260
tgagaagtga ggttttatca tcatctctca cgtttatctta tttggtccccca gccactattt 1320
agaattaatg gttaaagctt 1339

<210> 31

<211> 968

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Papaya AJ000923

<400> 31

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agaggcagaa tgcccaagt tgtagtttgc ggtaaaaagg tgttggaga aggagagtgt 660
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- 22 -

tgtggtgacg tcaatttctt gtgtgttgta ggcaaatcat atttgaataa aatctttctt 960
tcatatgt 968

<210> 32

<211> 1040

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Spruce AF051214

<400> 32

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aggttactaa tttagttta atagaccagg agaagatgcc gctgttaagc acatggatga 660
atcgattctg tgaggccat ggagtgaaag acgttatgcc ggatccggcc aagttgcagg 720
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ttggatttgc agagaatgga 1040

<210> 33

<211> 902

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Wheat AF004358

<400> 33

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acactgacac acatcgatcg aggtagttag agatggccgg aggagatgac ctgaagctgc 120
tcggcgcattt gccaagccca ttgttacca gggtaagct ggcgctcgcc ctgaaggccc 180

- 23 -

tgagctacga ggacgtggag gaggacctgt acaagaagag ttagcttctc ctcaagtcca 240
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agtgagccgc cagcacatat ccagaataat taaaatttgt tattttaaat gttgtttgtt 840
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<210> 34

<211> 1127

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Spruce AF051238

<400> 34

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cctgttcaat gtgcgtgtat tttagttgaa taagttttt atgaatctcg cttgtactgt 1080
agctatgtgc gatgattttt aatgccatag aaacgagaat gaaatgc 1127

- 24 -

<210> 35

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 35

gagagaggat cctcgagttt tttttttttt tttt

34

<210> 36

<211> 234

<212> PRT

<213> Glycine max

<400> 36

Met Ser Lys Ser Glu Asp Leu Lys Leu Leu Gly Gly Trp Phe Ser Pro
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Phe Ala Leu Arg Val Gln Ile Ala Leu Asn Leu Lys Gly Leu Glu Tyr
20 25 30

Glu Val Val Glu Glu Thr Leu Asn Pro Lys Ser Asp Leu Leu Leu Lys
35 40 45

Ser Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys
50 55 60

Val Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Ala Trp
65 70 75 80

Thr Asn Val Pro Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn
85 90 95

Ala Arg Phe Trp Phe Ala Tyr Ile Asp Glu Lys Trp Phe Thr Ser Leu
100 105 110

Arg Ser Val Leu Val Ala Glu Asp Asp Glu Ala Lys Lys Pro His Phe
115 120 125

Glu Gln Ala Glu Glu Gly Leu Glu Arg Leu Glu Glu Val Phe Asn Lys
130 135 140

- 25 -

Tyr Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Ser Ile Gly Phe Ile
145 150 155 160

Asp Ile Gly Phe Gly Ser Phe Leu Ser Trp Met Arg Val Ile Glu Glu
165 170 175

Met Ser Gly Arg Lys Leu Leu Asp Glu Lys Lys His Pro Gly Leu Thr
180 185 190

Gln Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Ile Leu
195 200 205

Pro Glu Thr Asp Lys Leu Val Glu Phe Ala Lys Ile Leu Gln Leu Lys
210 215 220

Trp Thr Ala Ala Ala Ala Ala Ala Lys
225 230

<210> 37
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<212> PRT
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<400> 37
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Pro Phe Leu His Arg Val Gln Ile Ala Leu Lys Leu Lys Gly Val Glu
20 25 30

Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu
35 40 45

Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu
50 55 60

Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr
65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu
85 90 95

- 26 -

Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala
100 105 110

Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Ala Lys
115 120 125

Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly
130 135 140

Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val
145 150 155 160

Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser
165 170 175

Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His
180 185 190

Pro Val Val Asn Glu Val Met Pro Pro Lys Asp Gln Leu Phe Ala Tyr
195 200 205

Phe Lys Ala Arg Ala Gln Ser Phe Val Ala Lys Arg Lys Asn
210 215 220

<210> 38

<211> 895

<212> DNA

<213> Glycine max

<400> 38

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gtctagaata tgaggttgtt gaagagacct tgaatccaa aagtgacctg cttcttaagt 180
ccaaaccctgt gcacaagaaa atcccaagtt tcttccatgg agataaagtc atttgtaat 240
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aaaatgctta tgatcgtgct aatgctcgat tttggtttgc ctacattgtat gagaagtgg 360
ttacgtcctt gagaagtgtt ctatggctg aagatgtatgg ggcaaaagaag ccacactttg 420
agcaagcaga agaagggttttgg aagaagtgtt caacaagtac agtgaaggaa 480
aggccttattt cggaggagat agcattggat tcattgacat tggtttggg agcttcttga 540
gttggatgag agtcatagag gagatgagtg gaagaaaaatt gcttcatgaa aagaagcacc 600
ctggtttgcac ccaatggctt gaaacgttttgc ctgctgatcc tgctgtgaag ggcattttc 660

- 27 -

cagagactga taagttgtt gagtttgcca agattcttca gctaaaatgg actgctgcag 720
cagctgcagc tgcaaagtaa atggaatcaa attaattgcg agagtatttt caaaattgtt 780
gtccaaaggttt ttttatctc aggctatgtt gttgcaactt tatttattta aaagttattt 840
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<210> 39

<211> 895

<212> DNA

<213> Glycine max

<400> 39

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agattgtctc caagttgaag ggagttgaat acaaataattt ggaagacgt ttgaacaaca 180
agagtgattt gctcctcaag tataacccag tttacaaaat gattccagtg cttgttcaca 240
atgagaagcc catttcagag tcccttgtga ttgttgagta cattgtatgac acatggaaaa 300
acaatcccat ctgccttct gatccctacc aaagagcctt ggctcgtttc tgggctaagt 360
tcattgtatga caagtgtgtg gttccagcat gaaaaatctgc ttttatgact gatgagaaag 420
agaaaagagaa ggctaaagaa gagttatttgg aggctctgag ttttcttgag aatgagttga 480
agggcaagtt ttttggtgga gaggagtttgg ctttggatgaa tattgctgct gtgttaatac 540
ctataattca agagatagca gggttcaat tgttcacaag tgagaaattc ccaaagctct 600
ctaaatggag ccaagacttt cacaaccatc cagttgtcaa cgaagttatg cctcctaagg 660
atcaactttt tgccattttc aaggctcggg ctcaaagctt cgttgctaaa agaaaagaatt 720
aatatagtga gactcagaat ttccatcgag gtttcagttt tttatgaaat gaaagctact 780
tgtctatgtt tcgttattgc ggttgtattt tcattttca atgaattatg tgatataatgg 840
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<210> 40

<211> 977

<212> DNA

<213> Glycine max

<400> 40

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caactatagtt gttctgttag aagtgtaca aacaacaatg gctgctaattc aggaagatgt 120
gaagcttttg ggagctactg gaagcccatt tgggtgcagg gttcagatttgc ccctcaagtt 180
gaaggggagtt caatacaaataat ttttggaaaga aaatttgagg aacaagagtg aactgcttct 240
caaatccaac ccagttcaca agaagggttcc agtgtttatt cacaatgaga agcccatagc 300
agagtctctt gtgattgttg aatacattga tgagacatgg aagaacaacc ccatcttgcc 360
ttctgatcct taccaaagag ccttggctcg tttctggtcc aaattcatttgc atgacaaggt 420
tgtgggtgct gcatggaaat atatttatac tggtgtatgag aaagagcgtg agaagaatgt 480
tgaagagtca tatgaggctc tgcagtttct tgagaatgag ctgaaggaca agaagttttt 540
tggaggagag gaaattgggt tggttagatat tgctgctgtc ttcatagcat ttggatcccc 600

- 28 -

tataattcaa gaagtattgg gttgaagtt attcacaagt gagaaatttc ctaagctcta 660
caaatgggc caagagtca tcaaccaccc tggtgtcaaa caagtccttc ctcccttagaga 720
tcaactttt gccttctaca aagcctgcca taaaagtctt tctgcttcaa aatagactta 780
tttaaggata gttgtgtcaa ctactggctc ctcatttg agttattgca gttgaattt 840
catgtcaatt tggtttata taaaatttag taacctggga tatctccat ggagaaaata 900
atcctggat cttgtttcca tttggccat ttcaagttaa aaagaaaattc atttttcca 960
aaaaaaaaaaaaaaa 977

<210> 41

<211> 1006

<212> DNA

<213> Glycine max

<400> 41

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aagaaaattt gaggaacaag agtgaactgc ttctcaaatac caacccagtt cacaagaagg 180
ttccagtgtt tattcacaat gagaagccca tagcagagtc tctgtgatt gttgaataca 240
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tcacagctga tgagaaagag cgtgagaaga atgttgagga agcaattgag ctctgcagtt 420
tcttgagaat gagataaagg acaagaagtt ctttgagga gaggagattt ggttggtaga 480
tattgctgct gtctacatag cattttgggt ccctatggtt caagaaaattt cagggttgg 540
gttattcaca agtgagaaat ttccataagct ccacaattgg agccaagaat tttgaacca 600
tccaattgtc aaagaaaatgc tgccccctag agatcctgtt ttctcccttt tcaagggtct 660
ctatgaaagc cttttgggt caaaatagat ttgatgatgt ggtgtgagac ttagtatttc 720
taagaattat gtgtttgtta aaggcttcta tgaaagcctc actgcttcaa aatagattca 780
tgtatgtgag actcagaatc tctggggaaa attgtgtgtg gtgtggacta cttgtttgt 840
ttgtcattga gctatatcgc tgttaatttag gatttgttt caaaatgatg cttataagtt 900
gtaatctagg atttctccct ttgaaatcct aggttgtct tgacatttgc tatttcaaag 960
aataaatata tagcatctt ctatttctca aaaaaaaaaaaaaaaa 1006

<210> 42

<211> 885

<212> DNA

<213> Glycine max

<400> 42

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acttggaaaa taagagtat ttgcttctaa agtacaaccc tgttcacaag aaggttcctg 180
tacttgttca taatggaaag gccattgctg aatccatggt gatccttgag tatattgatg 240
aaacatggaa agatggcct aaactgcttc caagtgattc ttacaaacga gcccaagctc 300

- 29 -

gattctggtg tcatttcatc caggatca gtaatggagag cactttcta gtatgtcaaaa 360
ctgatggaga agcacaacaa aaggccattg accacgtgt tgagaaaactg aaagtgcgtag 420
aagatgaaat gaagacctat ctgggagaag gcaatgctat tatctcttgtt gttgaaaaca 480
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aagttattgg cctcaagttc atagtgccag aaaagttcc tgtgttgtt tcttgggttga 600
tggctattgc tgaggttcaa gctgtgaaaa ttgcaactcc tccacatgaa aaaacagtgg 660
gaattcttca gttgttcagg ctgtctgcac tgaaatcttc ttctgccaca gaatgtatata 720
tacttcaaca cttaaataga ctgtccatcg ttgttgttctt ctgcgagtct tttagtgtatg 780
tatcttcaa taacaggatg agtaaacacct gagtatgtaa agcgtgtatga tatagagata 840
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<210> 43

<211> 991

<212> DNA

<213> Artificial Sequence

<400> 43

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ttgcaacaca attcaatttt gagcacttac caacaccact tccaatggct tcataatcatg 120
aagaagaagt gaggctattt ggcaagtggg ccagcccatt tagaacaga gttagacctt 180
ctctcaagct caagggtgtt ccctacaaat actccgagga agatcttgct aacaagagt 240
ctgatcttct caagtacaaac cccgttcaca agaaggttcc ggaaaaatggc cacaatggg 300
accattgcc cgagtcactc atcattgtt aatacataga tgagacgtgg aaaaataacc 360
caacttgc tcaagaccca tatgaaagag cttggctcg tttttggct aagaccttag 420
atgacaagat ctggccagct atatggaatg cttgctggag tgacgagaat gggcgtgaga 480
aaggcagtgg aagaaggcattt gaagcattga aaatcctaca ggaacacactg aaagacaaga 540
aattcttgg aggagagagc ataggattgg tagatattgc tgccaatttc attgggtatt 600
gggttgcattt attgcaagag attgcagggt tggagttgt caccatttagaaatccc 660
agttatataa ttggagtcaa gactttatca accaccctgt gatcaaggag ggtctgcctc 720
ctagagatga attgtttgtt ttcttcaaag cttctgctaa aaagtagaaac catttttagag 780
gttaggattca taataagttt gtatgatttt gttggaaac aattatcttgg ttgtgagcaa 840
aggattgttc tggatatttttaat ttaattgact gtgatattgg tgggtattgg ctatatttaat 900
tttaactaaa aaaagtgttc agtttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 991